

IT IS CLAIMED:

1. A transgenic plant comprising a plant transformation vector comprising a nucleotide sequence that encodes or is complementary to a sequence that encodes a PRDT1 polypeptide comprising the amino acid sequence of SEQ ID NO:2, or an ortholog thereof, wherein said transgenic plant has increased resistance to pathogens and/or increased drought tolerance relative to control plants.
2. The transgenic plant of claim 1 wherein the transformation vector comprises a constitutive promoter that controls expression of the PRDT1 polypeptide or ortholog.
3. The transgenic plant of claim 1 wherein the transformation vector comprises a pathogen-inducible promoter that controls expression of the PRDT1 polypeptide or ortholog.
4. The transgenic plant of claim 1 which encodes a PRDT1 ortholog comprising an amino acid sequence selected from any one of SEQ ID NOs:3-17.
5. A method of producing increased pathogen resistance in a plant, said method comprising:
 - a) introducing into progenitor cells of the plant a plant transformation vector comprising a nucleotide sequence that encodes or is complementary to a sequence that encodes a PRDT1 polypeptide comprising the amino acid sequence of SEQ ID NO:2, or an ortholog thereof, and
 - b) growing the transformed progenitor cells to produce a transgenic plant, wherein said polynucleotide sequence is expressed, and said transgenic plant exhibits increased resistance to pathogens relative to control plants.
6. A plant obtained by a method of claim 5.
7. A plant part obtained from a plant according to claim 6.

8. A method of generating a plant having an increased pathogen resistance and/or drought tolerance phenotype comprising identifying a plant that has an allele in its PRDT1 gene that results in increased pathogen resistance and/or drought tolerance compared to plants lacking the allele and generating progeny of said identified plant, wherein the generated progeny inherit the allele and have the increased pathogen resistance phenotype.
9. The method of claim 8 that employs candidate gene/QTL methodology.
10. The method of claim 8 that employs TILLING methodology.